Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup)** that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 25, 2005, 11:02:02 ; Search time 175 Seconds
(without alignments)
553.046 Million cell updates/sec

Title: US-09-823-077C-7
Perfect score: 1085
Sequence: 1 DSWWTSLNFLGGTTVCLGQN.....GPSLYSILSPFSPLLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1060	97.7	226	2	Q6XGG8	Q6xgg8 hepatitis b
2	1060	97.7	226	2	Q8BAN9	Q8ban9 hepatitis b
3	1060	97.7	281	2	Q6XGG9	Q6xgg9 hepatitis b
4	1060	97.7	389	2	Q6XGH0	Q6xgh0 hepatitis b
5	1054	97.1	222	2	Q9DIT9	Q9dit9 hepatitis b
6	1054	97.1	222	2	Q9DIV5	Q9div5 hepatitis b
7	1054	97.1	226	2	Q69601	Q69601 hepatitis b
8	1054	97.1	226	2	Q8BAM3	Q8bam3 hepatitis b
9	1054	97.1	226	2	Q8BAN5	Q8ban5 hepatitis b
10	1054	97.1	226	2	Q8BAP8	Q8bap8 hepatitis b
11	1054	97.1	226	2	Q9PX80	Q9px80 hepatitis b
12	1054	97.1	281	2	O41762	O41762 hepatitis b
13	1054	97.1	281	2	Q6XGJ0	Q6xgj0 hepatitis b
14	1054	97.1	281	2	Q9J1J6	Q9j1j6 hepatitis b
15	1054	97.1	281	2	Q9J1J7	Q9j1j7 hepatitis b
16	1054	97.1	281	2	Q9PWY5	Q9pwy5 hepatitis b
17	1054	97.1	337	2	Q70BE2	Q70be2 hepatitis b
18	1054	97.1	389	2	Q96843	Q96843 hepatitis b
19	1054	97.1	389	2	Q67871	Q67871 hepatitis b
20	1054	97.1	389	2	Q67879	Q67879 hepatitis b
21	1054	97.1	389	2	Q6XGJ1	Q6xgj1 hepatitis b
22	1054	97.1	389	2	Q7T4U0	Q7t4u0 hepatitis b
23	1054	97.1	389	2	Q7T4U6	Q7t4u6 hepatitis b
24	1054	97.1	389	2	Q9PWW6	Q9pww6 hepatitis b
25	1054	97.1	389	2	Q9WJC4	Q9wjc4 hepatitis b
26	1054	97.1	400	2	Q80J12	Q80j12 hepatitis b
27	1051	96.9	226	2	Q8BAM9	Q8bam9 hepatitis b
28	1050	96.8	222	2	Q9DIU9	Q9diu9 hepatitis b
29	1050	96.8	226	2	Q8AZ60	Q8az60 hepatitis b
30	1050	96.8	281	2	O41750	O41750 hepatitis b
31	1050	96.8	281	2	O41751	O41751 hepatitis b
32	1050	96.8	281	2	Q8AYU2	Q8ayu2 hepatitis b
33	1050	96.8	370	2	Q8AZ54	Q8az54 hepatitis b
34	1050	96.8	389	2	Q7T4V2	Q7t4v2 hepatitis b
35	1050	96.8	389	2	Q9IF39	Q9if39 hepatitis b
36	1049	96.7	226	2	Q67910	Q67910 hepatitis b
37	1049	96.7	226	2	Q6XGK3	Q6xgk3 hepatitis b
38	1049	96.7	226	2	Q8BAM5	Q8bam5 hepatitis b
39	1049	96.7	226	2	Q9Q3D5	Q9q3d5 hepatitis b
40	1049	96.7	226	2	Q9QAF5	Q9qaf5 hepatitis b
41	1049	96.7	281	2	Q67915	Q67915 hepatitis b
42	1049	96.7	281	2	Q6XGK4	Q6xgk4 hepatitis b
43	1049	96.7	281	2	Q9QAF1	Q9qaf1 hepatitis b
44	1049	96.7	382	2	Q67886	Q67886 hepatitis b
45	1049	96.7	389	2	Q67914	Q67914 hepatitis b

ALIGNMENTS

RESULT 1
Q6XGG8
ID Q6XGG8 PRELIMINARY; PRT; 226 AA.
AC Q6XGG8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE S protein.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15105537; DOI=10.1099/vir.0.19749-0;
RA Kimbi G.C., Kramvis A., Kew M.C.;
RT "Distinctive sequence characteristics of subgenotype A1 isolates of
RT hepatitis B virus from South Africa.";
RL J. Gen. Virol. 85:1211-1220(2004).
DR EMBL; AY233296; AAP79871.1; -.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; vMSA; 1.
KW Antigen.
SQ SEQUENCE 226 AA; 25361 MW; 228209EE5D7D204D CRC64;

Query Match 97.7%; Score 1060; DB 2; Length 226;
Best Local Similarity 97.4%; Pred. No. 2e-82;
Matches 184; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 SPLLPIFFC 221
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RESULT 2
Q8BAN9
ID Q8BAN9 PRELIMINARY; PRT; 226 AA.
AC Q8BAN9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface antigen.

```
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bowden R.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
RA   Locarnini S., Carman W.F.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY122559; AAM82961.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   226 AA;  25361 MW;  228209F95608229D CRC64;

  Query Match             97.7%;  Score 1060;  DB 2;  Length 226;
  Best Local Similarity   97.4%;  Pred. No. 2e-82;
  Matches  184;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 3
Q6XGG9
ID   Q6XGG9      PRELIMINARY;      PRT;   281 AA.
AC   Q6XGG9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Middle S protein.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15105537; DOI=10.1099/vir.0.19749-0;
RA   Kimbi G.C., Kramvis A., Kew M.C.;
RT   "Distinctive sequence characteristics of subgenotype A1 isolates of
RT   hepatitis B virus from South Africa.";
RL   J. Gen. Virol. 85:1211-1220(2004).
DR   EMBL; AY233296; AAP79872.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   281 AA;  31206 MW;  E95FEC6AD353604F CRC64;

  Query Match             97.7%;  Score 1060;  DB 2;  Length 281;
  Best Local Similarity   97.4%;  Pred. No. 2.4e-82;
  Matches  184;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 SPLLPIFFC 276


RESULT 4
Q6XGH0
ID   Q6XGH0      PRELIMINARY;      PRT;   389 AA.
AC   Q6XGH0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Large S protein.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15105537; DOI=10.1099/vir.0.19749-0;
RA   Kimbi G.C., Kramvis A., Kew M.C.;
RT   "Distinctive sequence characteristics of subgenotype A1 isolates of
RT   hepatitis B virus from South Africa.";
RL   J. Gen. Virol. 85:1211-1220(2004).
DR   EMBL; AY233296; AAP79867.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   389 AA;  42691 MW;  CEE26773DFC603F2 CRC64;

  Query Match             97.7%;  Score 1060;  DB 2;  Length 389;
  Best Local Similarity   97.4%;  Pred. No. 3.3e-82;
  Matches  184;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 SPLLPIFFC 384


RESULT 5
Q9DIT9
ID   Q9DIT9      PRELIMINARY;      PRT;   222 AA.
AC   Q9DIT9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Surface antigen (Fragment).
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu H.F.;
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RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ297881; CAC20278.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
FT   NON_TER     222    222
SQ   SEQUENCE   222 AA;  24825 MW;  9D65834D72D4EFD3 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 222;
  Best Local Similarity   96.8%;  Pred. No. 6.4e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 6
Q9DIV5
ID   Q9DIV5      PRELIMINARY;      PRT;   222 AA.
AC   Q9DIV5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Surface antigen (Fragment).
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu H.F.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ297865; CAC20262.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
FT   NON_TER     222    222
SQ   SEQUENCE   222 AA;  24825 MW;  9D65834D72D4EFD3 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 222;
  Best Local Similarity   96.8%;  Pred. No. 6.4e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 7
Q69601
ID   Q69601      PRELIMINARY;      PRT;   226 AA.
AC   Q69601;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   S gene subtype ayw2 protein.
GN   Name=S gene subtype ayw2;
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=genotype D;
RX   MEDLINE=92268879; PubMed=1588323;
RA   Norder H., Hammas B., Lfdahl S., Courouc A.M., Magnius L.O.;
RT   "Comparison of the amino acid sequences of nine different serotypes of
RT   Hepatitis B surface antigen and genomic classification of the
RT   corresponding hepatitis B virus strains.";
RL   J. Gen. Virol. 73:1201-1208(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=genotype D;
RA   Norder H.M.L.;
RL   Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X75662; CAA53349.1; -.
DR   PIR; JQ1571; JQ1571.
DR   PIR; JQ1572; JQ1572.
DR   PIR; JQ2063; JQ2063.
DR   PIR; JQ2066; JQ2066.
DR   PIR; JQ2067; JQ2067.
DR   PIR; JQ2068; JQ2068.
DR   PIR; JQ2069; JQ2069.
DR   PIR; JQ2070; JQ2070.
DR   PIR; JQ2072; JQ2072.
DR   PIR; JQ2076; JQ2076.
DR   PIR; JQ2077; JQ2077.
DR   PIR; JQ2079; JQ2079.
DR   PIR; JQ2081; JQ2081.
DR   PIR; JQ2083; JQ2083.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   226 AA;  25460 MW;  C88303545C6838E6 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 226;
  Best Local Similarity   96.8%;  Pred. No. 6.5e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 8
Q8BAM3
ID   Q8BAM3      PRELIMINARY;      PRT;   226 AA.
AC   Q8BAM3;
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DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Surface antigen.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bowden R.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
RA   Locarnini S., Carman W.F.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY122567; AAM82977.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   226 AA;  25359 MW;  9C60B38B9DFDC928 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 226;
  Best Local Similarity   96.8%;  Pred. No. 6.5e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 9
Q8BAN5
ID   Q8BAN5      PRELIMINARY;      PRT;   226 AA.
AC   Q8BAN5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Surface antigen.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bowden R.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
RA   Locarnini S., Carman W.F.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY122561; AAM82965.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   226 AA;  25387 MW;  B4D69BF2A6626A43 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 226;
  Best Local Similarity   96.8%;  Pred. No. 6.5e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 10
Q8BAP8
ID   Q8BAP8      PRELIMINARY;      PRT;   226 AA.
AC   Q8BAP8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Surface antigen.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bowden R.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
RA   Locarnini S., Carman W.F.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY122552; AAM82947.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   226 AA;  25374 MW;  465EEE830BB0EE1D CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 226;
  Best Local Similarity   96.8%;  Pred. No. 6.5e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 11
Q9PX80
ID   Q9PX80      PRELIMINARY;      PRT;   226 AA.
AC   Q9PX80;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   S protein (Major surface antigen).
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20109034; PubMed=10640544;
RA   Hannoun C., Horal P., Lindh M.;
RT   "Long-term mutation rates in the hepatitis B virus genome.";
RL   J. Gen. Virol. 81:75-83(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=438;
RX   MEDLINE=20345625; PubMed=10884611; DOI=10.1016/S1286-4579(00)00365-8;
RA   Borchani-Chabchoub I., Gargouri A., Mokdad-Gargouri R.;
RT   "Genotyping of Tunisian hepatitis B virus isolates based on the
RT   sequencing of preS2 and S regions.";
RL   Microbes Infect. 2:607-612(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Bowden R.J.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
RA   Locarnini S., Carman W.F.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   PubMed=15105537; DOI=10.1099/vir.0.19749-0;
RA   Kimbi G.C., Kramvis A., Kew M.C.;
RT   "Distinctive sequence characteristics of subgenotype A1 isolates of
RT   hepatitis B virus from South Africa.";
RL   J. Gen. Virol. 85:1211-1220(2004).
DR   EMBL; AF121241; AAF24676.1; -.
DR   EMBL; AF229159; AAF40187.1; -.
DR   EMBL; AY122553; AAM82949.1; -.
DR   EMBL; AY122554; AAM82951.1; -.
DR   EMBL; AY122557; AAM82957.1; -.
DR   EMBL; AY122558; AAM82959.1; -.
DR   EMBL; AY122568; AAM82979.1; -.
DR   EMBL; AY122589; AAM83021.1; -.
DR   EMBL; AY233293; AAP79850.1; -.
DR   EMBL; AF121240; AAF24669.1; -.
DR   PIR; JQ1572; JQ1572.
DR   PIR; JQ2063; JQ2063.
DR   PIR; JQ2066; JQ2066.
DR   PIR; JQ2067; JQ2067.
DR   PIR; JQ2068; JQ2068.
DR   PIR; JQ2069; JQ2069.
DR   PIR; JQ2070; JQ2070.
DR   PIR; JQ2072; JQ2072.
DR   PIR; JQ2076; JQ2076.
DR   PIR; JQ2077; JQ2077.
DR   PIR; JQ2079; JQ2079.
DR   PIR; JQ2081; JQ2081.
DR   PIR; JQ2083; JQ2083.
DR   PIR; JQ2091; JQ2091.
DR   PIR; JQ2092; JQ2092.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   226 AA;  25387 MW;  228209EE5D65834D CRC64;

  Query Match           97.1%;  Score 1054;  DB 2;  Length 226;
  Best Local Similarity   96.8%;  Pred. No. 6.5e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 12
O41762
ID   O41762      PRELIMINARY;      PRT;   281 AA.
AC   O41762;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Middle S protein.
GN   Name=preS2/S;
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97368435; PubMed=9225049;
RA   Bowyer S., van Staden L., Kew M.C., Sim J.G.;
RT   "A unique segment of the hepatitis B virus group A genotype identified
RT   in isolates from South Africa.";
RL   J. Gen. Virol. 78:1719-1729(1997).
DR   EMBL; U87851; AAC58030.1; -.
DR   PIR; JQ1572; JQ1572.
DR   PIR; JQ2063; JQ2063.
DR   PIR; JQ2066; JQ2066.
DR   PIR; JQ2067; JQ2067.
DR   PIR; JQ2068; JQ2068.
DR   PIR; JQ2069; JQ2069.
DR   PIR; JQ2070; JQ2070.
DR   PIR; JQ2072; JQ2072.
DR   PIR; JQ2076; JQ2076.
DR   PIR; JQ2077; JQ2077.
DR   PIR; JQ2079; JQ2079.
DR   PIR; JQ2081; JQ2081.
DR   PIR; JQ2083; JQ2083.
DR   PIR; JQ2091; JQ2091.
DR   PIR; JQ2092; JQ2092.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   281 AA;  31338 MW;  74ADAD08E3491BC9 CRC64;

  Query Match           97.1%;  Score 1054;  DB 2;  Length 281;
  Best Local Similarity   96.8%;  Pred. No. 7.9e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
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Db        268 LPLLPIFFC 276


RESULT 13
Q6XGJ0
ID   Q6XGJ0      PRELIMINARY;      PRT;   281 AA.
AC   Q6XGJ0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Middle S protein.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15105537; DOI=10.1099/vir.0.19749-0;
RA   Kimbi G.C., Kramvis A., Kew M.C.;
RT   "Distinctive sequence characteristics of subgenotype A1 isolates of
RT   hepatitis B virus from South Africa.";
RL   J. Gen. Virol. 85:1211-1220(2004).
DR   EMBL; AY233293; AAP79851.1; -.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
SQ   SEQUENCE   281 AA;  31232 MW;  52325AB26590AEF8 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 281;
  Best Local Similarity   96.8%;  Pred. No. 7.9e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 14
Q9J1J6
ID   Q9J1J6      PRELIMINARY;      PRT;   281 AA.
AC   Q9J1J6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PreS2-S protein.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1344b;
RX   MEDLINE=20345625; PubMed=10884611; DOI=10.1016/S1286-4579(00)00365-8;
RA   Borchani-Chabchoub I., Gargouri A., Mokdad-Gargouri R.;
RT   "Genotyping of Tunisian hepatitis B virus isolates based on the
RT   sequencing of preS2 and S regions.";
RL   Microbes Infect. 2:607-612(2000).
DR   EMBL; AF214661; AAF31270.1; -.
DR   PIR; JQ1572; JQ1572.
DR   PIR; JQ2063; JQ2063.
DR   PIR; JQ2066; JQ2066.
DR   PIR; JQ2067; JQ2067.
DR   PIR; JQ2068; JQ2068.
DR   PIR; JQ2069; JQ2069.
DR   PIR; JQ2070; JQ2070.
DR   PIR; JQ2072; JQ2072.
DR   PIR; JQ2076; JQ2076.
DR   PIR; JQ2077; JQ2077.
DR   PIR; JQ2079; JQ2079.
DR   PIR; JQ2081; JQ2081.
DR   PIR; JQ2083; JQ2083.
DR   PIR; JQ2091; JQ2091.
DR   PIR; JQ2092; JQ2092.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
FT   CHAIN        56    272       S protein.
SQ   SEQUENCE   281 AA;  31270 MW;  673BC6C4902BF954 CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 281;
  Best Local Similarity   96.8%;  Pred. No. 7.9e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 15
Q9J1J7
ID   Q9J1J7      PRELIMINARY;      PRT;   281 AA.
AC   Q9J1J7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PreS2-S protein.
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=926h;
RX   MEDLINE=20345625; PubMed=10884611; DOI=10.1016/S1286-4579(00)00365-8;
RA   Borchani-Chabchoub I., Gargouri A., Mokdad-Gargouri R.;
RT   "Genotyping of Tunisian hepatitis B virus isolates based on the
RT   sequencing of preS2 and S regions.";
RL   Microbes Infect. 2:607-612(2000).
DR   EMBL; AF214660; AAF31269.1; -.
DR   PIR; JQ1572; JQ1572.
DR   PIR; JQ2063; JQ2063.
DR   PIR; JQ2066; JQ2066.
DR   PIR; JQ2067; JQ2067.
DR   PIR; JQ2068; JQ2068.
DR   PIR; JQ2069; JQ2069.
DR   PIR; JQ2070; JQ2070.
DR   PIR; JQ2072; JQ2072.
DR   PIR; JQ2076; JQ2076.
DR   PIR; JQ2077; JQ2077.
DR   PIR; JQ2079; JQ2079.
DR   PIR; JQ2081; JQ2081.
DR   PIR; JQ2083; JQ2083.
DR   PIR; JQ2091; JQ2091.
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DR   PIR; JQ2092; JQ2092.
DR   GO; GO:0016032; P:viral life cycle; IEA.
DR   InterPro; IPR000349; Hepvir_surfAg.
DR   Pfam; PF00695; vMSA; 1.
KW   Antigen.
FT   CHAIN        56    281       S protein.
SQ   SEQUENCE   281 AA;  31260 MW;  F2325C86F7D9844E CRC64;

  Query Match             97.1%;  Score 1054;  DB 2;  Length 281;
  Best Local Similarity   96.8%;  Pred. No. 7.9e-82;
  Matches  183;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


Search completed: July 25, 2005, 11:24:29
Job time : 176 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 25, 2005, 11:01:26 ; Search time 164 Seconds
(without alignments)
445.718 Million cell updates/sec

Title: US-09-823-077C-7
Perfect score: 1085
Sequence: 1 DSWWTSLNFLGGTTVCLGQN.....GPSLYSILSPFSPLLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1054	97.1	229	6	ABP55076	Abp55076 Hepatitis
2	1054	97.1	347	3	AAB10596	Aab10596 HBV fusio
3	1046	96.4	226	4	AAG62930	Aag62930 Amino aci
4	1046	96.4	309	7	ADG76903	Adg76903 Hepatitis
5	1046	96.4	389	4	AAG66931	Aag66931 HBV genot
6	1046	96.4	389	4	AAG62931	Aag62931 Amino aci
7	1045	96.3	226	2	AAW62826	Aaw62826 Hepatitis
8	1043	96.1	226	7	ADC06672	Adc06672 HBV envel
9	1041	95.9	226	7	ADG76900	Adg76900 Hepatitis
10	1040	95.9	226	5	AAE19897	Aae19897 Hepatitis
11	1040	95.9	226	7	ABW00348	Abw00348 Hepatitis
12	1040	95.9	249	3	AAY52545	Aay52545 Pan DR ep
13	1040	95.9	281	2	AAR27471	Aar27471 spsAg pro
14	1040	95.9	281	2	AAY32835	Aay32835 HBsAg Pre
15	1040	95.9	309	7	ADG76901	Adg76901 Hepatitis
16	1040	95.9	309	7	ADG76902	Adg76902 Hepatitis
17	1040	95.9	334	5	AAO22926	Aao22926 HbsAg-EE7
18	1040	95.9	389	2	AAR27472	Aar27472 lpsAg pro
19	1040	95.9	389	2	AAR27474	Aar27474 I3L promo
20	1040	95.9	389	6	ABO10262	Abo10262 HBV major
21	1040	95.9	393	4	AAU14097	Aau14097 Hepatitis
22	1040	95.9	397	2	AAW09048	Aaw09048 Plasmid p
23	1037	95.6	226	1	AAP00042	Aap00042 Sequence
24	1037	95.6	226	2	AAR06613	Aar06613 Hepatitis
25	1037	95.6	371	7	ADN02610	Adn02610 HBV N-ter
26	1037	95.6	389	7	ADN02608	Adn02608 HBV preS1
27	1033	95.2	203	1	AAP10002	Aap10002 Sequence
28	1033	95.2	226	1	AAP10001	Aap10001 Sequence
29	1033	95.2	226	2	AAW09045	Aaw09045 Hepatitis
30	1033	95.2	229	6	ABP55075	Abp55075 Hepatitis
31	1033	95.2	276	2	AAW44780	Aaw44780 Modified
32	1033	95.2	389	6	ABP55073	Abp55073 Hepatitis
33	1031	95.0	226	1	AAP00005	Aap00005 Sequence
34	1031	95.0	226	1	AAP60374	Aap60374 Hepatitis
35	1030	94.9	226	5	ABB77764	Abb77764 Amino aci
36	1026	94.6	305	7	ADC06666	Adc06666 HBV envel
37	1014	93.5	325	7	ADG76917	Adg76917 Hepatitis
38	1010	93.1	309	7	ADG76918	Adg76918 Hepatitis
39	1009	93.0	197	7	ADG76914	Adg76914 Hepatitis
40	1007	92.8	226	2	AAR33252	Aar33252 HBsAg enc
41	1007	92.8	226	2	AAR55282	Aar55282 Deduced s
42	1007	92.8	251	2	AAR11495	Aar11495 RP135/HBs
43	1007	92.8	281	4	AAE02620	Aae02620 HBsAg pre
44	1007	92.8	389	2	AAR55287	Aar55287 Deduced s
45	1007	92.8	390	4	AAE02621	Aae02621 Chimeric

ALIGNMENTS

RESULT 1
ABP55076
ID ABP55076 standard; protein; 229 AA.
XX
AC ABP55076;
XX
DT 27-JAN-2003 (first entry)
XX
DE Hepatitis B virus wild-type small envelope protein.
XX
KW HBV; HBsAg; surface antigen; envelope; diagnosis; vaccine.
XX
OS Hepatitis b virus.
XX
PN WO200279217-A1.
XX
PD 10-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009227.
XX
PR 30-MAR-2001; 2001US-00821877.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Coleman PF, Mushahwar IA;
XX
DR WPI; 2003-040642/03.
DR N-PSDB; ABV75785.
XX
PT New nucleotide sequences, useful for detecting compounds that bind to
PT gp41 protein or antibodies to the Hepatitis B virus surface antigen
PT mutant or for creating primers and probes.
XX
PS Claim 3; Fig 4A-B; 43pp; English.
XX
CC The present sequence is the protein sequence of the small envelope
CC protein of a wild-type hepatitis B virus (HBV) subtype ayw2 strain. The
CC invention relates to a mutated HBV ayw1 strain isolated from a French
CC sample and identified as 990525169. The mutant sequence (see ABP55075)
CC contains 3 mutations compared with the wild-type sequence: substitution
CC of alanine for the threonine residue at position 123; tryptophan for
CC leucine-199; and serine for threonine-207. The T123A substitution is
CC within the 'a' determinant region and affects the H166 epitope. The
CC present invention relates to the novel HBV mutant which has a modified
CC 'a' determinant as a result of T123A amino acid substitution, and to
CC methods of detecting this mutant, and/or antibodies to the mutant, in
CC patient samples. The identification and detection of mutant HBV may lead
CC to improved vaccine development and detection systems

CX
SQ Sequence 229 AA;

Query Match 97.1%; Score 1054; DB 6; Length 229;
Best Local Similarity 96.8%; Pred. No. 1.2e-87;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 95

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         96 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 155

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        156 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 215

Qy        181 SPLLPIFFC 189
              |||||||||
Db        216 LPLLPIFFC 224
```

RESULT 2
AAB10596
ID AAB10596 standard; protein; 347 AA.
XX
AC AAB10596;
XX
DT 06-AUG-2003 (revised)
DT 08-JAN-2001 (first entry)
XX
DE HBV fusion protein comprising LHB and RGD.
XX
KW Fusion protein; protein coat; virus-specific packaging signal; psi;
KW virus protein; cell permeability; cell-specific binding site; LHB;
KW large surface protein; core antigen; gene therapy.
XX
OS Hepatitis B virus.
OS Synthetic.
XX
PN WO200046376-A2.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-DE000363.
XX
PR 05-FEB-1999; 99DE-01004800.
XX
PA (HILD/) HILDT E.
XX
PI Hildt E, Hofschneider P;
XX
DR WPI; 2000-514959/46.
DR N-PSDB; AAA71734.
XX
PT Particle for cell-specific gene delivery, useful in gene therapy,
PT comprises nucleic acid in protein coat that includes a fusion protein of
PT viral protein, permeability peptide and cell-binding site.
XX
PS Claim 14; Fig 1; 34pp; German.
XX
CC This invention describes a novel particle (A), comprising a protein coat
CC with a fusion protein (FP), and, inside the coat, a nucleic acid (I)
CC including the sequence for a virus-specific packaging signal (psi) and a
CC structural gene. FP contains a virus protein (VP), a peptide (P) that
CC mediates cell permeability and a heterologous cell-specific binding site
CC (RGD). The invention also describes (1) producing (A) in which FP
CC contains an LHBs (large surface protein of hepatitis B virus (HBV)) and
CC RGD; (2) preparing (A) in which FP contains an HBV core antigen (HBcAg),
CC (P) and RGD; (3) FP; (4) DNA encoding FP; and (5) expression vector
CC containing the DNA of (d). The products of the invention are used in gene
CC therapy of cells and tissues, in vivo or ex vivo. This sequence
CC represents a fusion protein which is described in the method of the
CC invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 347 AA;

Query Match 97.1%; Score 1054; DB 3; Length 347;
Best Local Similarity 96.8%; Pred. No. 1.9e-87;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 213

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        214 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 273

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        274 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 333

Qy        181 SPLLPIFFC 189
              |||||||||
Db        334 LPLLPIFFC 342
```

RESULT 3
AAG62930
ID AAG62930 standard; protein; 226 AA.
XX
AC AAG62930;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a mutated HBV S gene antigen.
XX
KW S gene; HBsm; mHVB; HBV; pre-S gene; C gene; P gene; X gene;
KW surface antigen; envelope protein; HBsAg; HBeAg; HBcAg; DNA polymerase;
KW reverse transcriptase; HBxAg; immune response; viral protein expression;
KW HBV infection.
XX
OS Hepatitis B virus.
XX
PN WO200149828-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-FR000038.
XX
PR 06-JAN-2000; 2000FR-00000129.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INMR) BIOMERIEUX SA.
XX
PI Trepo C, Mandrand B, Kay A, Chemin I, Komurian-Pradel F;
XX
DR WPI; 2001-441870/47.
XX
PT New mutant of hepatitis B virus, useful for diagnosis, prevention and
PT treatment of infection, also related nucleic acids, proteins and
PT antibodies.
XX
PS Claim 36; Page 92; 102pp; French.
XX
CC The present sequence represents a mutated S gene antigen, designated
CC HBsm. It is part of the mutant hepatitis B virus (mHVB) of the invention,
CC which has a circular, partially double-stranded genome comprising pre-S,
CC S, C, P and X genes, encoding, respectively, surface antigens, envelope
CC protein (HBsAg), proteins HBeAg and HBcAg, DNA polymerase/reverse
CC transcriptase, and HBxAg. The mutant HBV of the invention are used for
CC induction of specific humoral or cellular immune responses, or antisense
CC inhibition of viral protein expression. Proteins and nucleic acids

```
CC   derived from mHVB (also related antibodies, vectors, transformed cells
CC   and oligonucleotides) are useful for diagnosis (in standard
CC   amplification, hybridization or immune-complex forming assays) and for
CC   treatment of, or vaccination against, HBV infection
XX
SQ   Sequence 226 AA;

  Query Match             96.4%;  Score 1046;  DB 4;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 6.6e-87;
  Matches  181;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||:|| ||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYNILRPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 4
ADG76903
ID   ADG76903 standard; protein; 309 AA.
XX
AC   ADG76903;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Hepatitis B virus envelope amino acid sequence SeqID26.
XX
KW   hepatitis B virus; HBV; polymerase; ADV; LMV; TFV; FTC; ADV; LMV; ADV;
KW   TFV; anti-HBV agent; hepatotropic; virucide; antiinflammatory;
KW   HBV variant polymerase-antagonist; gene therapy; viral component;
KW   inhibiting infection; virus replication; virus release; envelope.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1. .309
FT                   /label= OTHER
FT                   /note= "OTHER= Any Xaa's in this sequence can be any
FT                   amino acid"
XX
PN   WO2003087351-A1.
XX
PD   23-OCT-2003.
XX
PF   11-APR-2003; 2003WO-AU000432.
XX
PR   12-APR-2002; 2002AU-00001710.
PR   26-JUN-2002; 2002AU-00003224.
XX
PA   (MELB-) MELBOURNE HEALTH.
PA   (AUST-) AUSTIN & REPATRIATION MEDICAL CENT.
PA   (SHEA-) SOUTHERN HEALTH.
XX
PI   Bartholomeusz AI,  Locarnini SA,  Ayres A,  Colledge D,  Sasadeusz J;
PI   Tillmann H,  Angus PW,  Sievert W;
XX
DR   WPI; 2003-845324/78.
XX
PT   New isolated hepatitis B viral variants with reduced susceptibility to
PT   nucleoside analogs, useful for screening, designing and/or developing
PT   agents capable of inhibiting infection, replication and/or release of the
PT   virus.
XX
PS   Example 5; SEQ ID NO 26; 268pp; English.
XX
CC   This invention relates to a novel isolated hepatitis B virus (HBV)
CC   variant which comprises a nucleoside mutation in a gene encoding a DNA
CC   polymerase resulting in at least one amino acid addition, substitution
CC   and/or deletion to the polymerase, and exhibiting decreased sensitivity
CC   to (for example) ADV, LMV, TFV, or FTC, or ADV and LMV, ADV and TFV,
CC   and/or other nucleoside, analogues, anti-HBV agents or their
CC   combinations. The invention may be useful for the development of
CC   compounds with a hepatotropic, virucide or antiinflammatory activity as
CC   HBV variant polymerase-antagonists. In addition, the sequences may be
CC   useful for gene therapy. The HBV variants or their component are useful
CC   in the rational design of an anti-HBV agent comprising microarray
CC   analysis and is based on the crystal structure or NMR structure of a
CC   viral component. The methods and compositions of the present invention
CC   are also useful for screening, designing and/or developing agents capable
CC   of inhibiting infection, replication and/or release of the virus.
XX
SQ   Sequence 309 AA;

  Query Match             96.4%;  Score 1046;  DB 7;  Length 309;
  Best Local Similarity   96.3%;  Pred. No. 9.1e-87;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 175

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:||||||||||||| | |||||| ||||||||||||||||||||||||||
Db        176 FLLVLLDYQGMLPVCPLIPGSSTTSAGTCRTCTTAAQGTSMYPSCCCTKPSDGNCTCIPI 235

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        236 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 295

Qy        181 SPLLPIFFC 189
              |||||||||
Db        296 LPLLPIFFC 304


RESULT 5
AAG66931
ID   AAG66931 standard; protein; 389 AA.
XX
AC   AAG66931;
XX
DT   19-OCT-2001  (first entry)
XX
DE   HBV genotype D preS1/preS2/HBsAg polypeptide.
XX
KW   Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
KW   HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBeAg.
XX
OS   Hepatitis B virus.
XX
PN   WO200140279-A2.
XX
PD   07-JUN-2001.
XX
PF   20-NOV-2000; 2000WO-EP011526.
XX
PR   03-DEC-1999;   99EP-00870252.
PR   07-DEC-1999;   99US-0169287P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Stuyver L,  Van Geyt C,  De Gendt S;
XX
DR   WPI; 2001-374785/39.
XX
PT   Novel isolated and/or purified hepatitis B virus polypeptide and
```

```
PT   polynucleotide sequences that are phylogenetically different from HBV
PT   genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
PT   therapy.
XX
PS   Example 3; Fig 6; 94pp; English.
XX
CC   The invention relates to the complete nucleic acid sequence of a new
CC   human hepatitis B virus (HBV) genotype, provisionally named genotype G.
CC   This genotype was found with a high prevalence in patients chronically
CC   infected with HBV and residing in Europe and the USA. The invention
CC   relates to a fully defined sequence of 3248 nucleotides as given in
CC   specification, a sequence with 92% identity to the given sequence, or
CC   sequence that is degenerate to the mentioned sequences. These
CC   polynucleotides are useful for HBV genotyping. The proteins encoded by
CC   the polynucleotides are useful for detecting antibodies in a biological
CC   sample. Ligands that bind to the proteins and antibodies directed against
CC   the proteins are useful for detecting the proteins and for detecting
CC   HBcAg and HBeAg (precore precursor proteins). They are also useful for
CC   preparing a vaccine or medicament for treating HBV infections. The
CC   present sequence is provided in an amino acid sequence alignment of the
CC   preS1, preS2 and HBsAg open reading frame of the different HBV genotypes
XX
SQ   Sequence 389 AA;

  Query Match             96.4%;  Score 1046;  DB 4;  Length 389;
  Best Local Similarity   96.3%;  Pred. No. 1.2e-86;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||| ||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSAGPCRTCTTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 6
AAG62931
ID   AAG62931 standard; protein; 389 AA.
XX
AC   AAG62931;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Amino acid sequence of a mutated HBV Pre-S protein.
XX
KW   S gene; HBsm; mHVB; HBV; pre-S gene; C gene; P gene; X gene;
KW   surface antigen; envelope protein; HBsAg; HBeAg; HBcAg; DNA polymerase;
KW   reverse transcriptase; HBxAg; immune response; viral protein expression;
KW   HBV infection.
XX
OS   Hepatitis B virus.
XX
PN   WO200149828-A1.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-FR000038.
XX
PR   06-JAN-2000; 2000FR-00000129.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (INMR ) BIOMERIEUX SA.
XX
PI   Trepo C,  Mandrand B,  Kay A,  Chemin I,  Komurian-Pradel F;
XX
DR   WPI; 2001-441870/47.
XX
PT   New mutant of hepatitis B virus, useful for diagnosis, prevention and
PT   treatment of infection, also related nucleic acids, proteins and
PT   antibodies.
XX
PS   Claim 36; Page 92-94; 102pp; French.
XX
CC   The present sequence represents a mutated Pre-S gene. It is part of the
CC   mutant hepatitis B virus (mHVB) of the invention, which has a circular,
CC   partially double-stranded genome comprising pre-S, S, C, P and X genes,
CC   encoding, respectively, surface antigens, envelope protein (HBsAg),
CC   proteins HBeAg and HBcAg, DNA polymerase/reverse transcriptase, and
CC   HBxAg. The mutant HBV of the invention are used for induction of specific
CC   humoral or cellular immune responses, or antisense inhibition of viral
CC   protein expression. Proteins and nucleic acids derived from mHVB (also
CC   related antibodies, vectors, transformed cells and oligonucleotides) are
CC   useful for diagnosis (in standard amplification, hybridization or immune-
CC   complex forming assays) and for treatment of, or vaccination against, HBV
CC   infection
XX
SQ   Sequence 389 AA;

  Query Match             96.4%;  Score 1046;  DB 4;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.2e-86;
  Matches  181;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:||||||||||||||| | ||||||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||:|| ||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYNILRPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 7
AAW62826
ID   AAW62826 standard; protein; 226 AA.
XX
AC   AAW62826;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Hepatitis B virus surface antigen.
XX
KW   Hepatitis delta virus; L-HDag; virus-like particle; infection;
KW   hepatitis B surface antigen; HBsAg; immunogen; vaccine.
XX
OS   Hepatitis B virus.
XX
PN   WO9828004-A1.
XX
PD   02-JUL-1998.
XX
PF   24-DEC-1997;   97WO-AU000884.
XX
PR   24-DEC-1996;   96AU-00004341.
XX
PA   (QUEE-) QUEENSLAND DEPT HEALTH SAKZEWSKI VIRUS.
XX
PI   Gowans EJ,  Macnaughton TB;
XX
```

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DR   WPI; 1998-377411/32.
DR   N-PSDB; AAV42306.
XX
PT   Virus-like particle for, e.g. treating microbial infection - comprises
PT   polypeptide from microorganism and sequence from Hepatitis D virus large
PT   protein, partially enveloped by Hepatitis B surface antigen.
XX
PS   Example; Fig 6; 72pp; English.
XX
CC   This polypeptide comprises a hepatitis B virus surface antigen (HBsAg)
CC   encoded by the DNA insert (see AAV42306) of plasmid pTBM-HBsAg. The
CC   invention provides a virus-like particle (VLP) comprising an antigenic
CC   and/or immunogenic polypeptide from a microorganism (e.g. hepatitis C
CC   virus) fused to at least the last 19 amino acids (see AAW62827) of the C-
CC   terminal sequence of the large protein from hepatitis D virus (L-HDag),
CC   in which the fusion protein is packaged into VLPs through the interaction
CC   of the L-HDAg moiety with HBsAg. The VLP is used to ameliorate or protect
CC   against infections caused by hepatitis B virus and/or another
CC   microorganism
XX
SQ   Sequence 226 AA;

  Query Match             96.3%;  Score 1045;  DB 2;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 8.1e-87;
  Matches  181;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              :|||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ESWWTSLNFLGGNTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        153 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 8
ADC06672
ID   ADC06672 standard; protein; 226 AA.
XX
AC   ADC06672;
XX
DT   18-DEC-2003  (first entry)
XX
DE   HBV envelope gene protein from patient B on-ETV therapy.
XX
KW   HBV; entecavir; ETV; lamivudine[(-)-beta-2'-deoxy-3'-thiacytidine];
KW   lamivudine; LMV; 3TC; virucide; antiinflammatory; hepatotropic;
KW   nucleoside analogue resistance; vaccine; HBsAg; envelope;
KW   surface antigen.
XX
OS   Hepatitis B virus.
XX
PN   WO2003066841-A1.
XX
PD   14-AUG-2003.
XX
PF   05-FEB-2003; 2003WO-AU000111.
XX
PR   07-FEB-2002; 2002AU-00000370.
PR   21-MAR-2002; 2002AU-00001269.
XX
PA   (MELB-) MELBOURNE HEALTH.
PA   (AUST-) AUSTIN & REPATRIATION MEDICAL CENT.
PA   (SHEA-) SOUTHERN HEALTH.
XX
PI   Bartholomeusz AI,  Locarnini SA,  Ayres A,  Angus PW,  Sievert W;
XX
DR   WPI; 2003-663592/62.
XX
PT   New variants of hepatitis B virus resistant to nucleoside analogs, useful
PT   in vaccines and for screening to detect therapeutic inhibitors.
XX
PS   Example 5; Fig 10; 124pp; English.
XX
CC   The invention relates to a novel isolated hepatitis B virus (HBV) variant
CC   comprising a nucleoside mutation in a DNA polymerase gene resulting in at
CC   least one amino acid addition, substitution and/or deletion, where the
CC   variant has reduced sensitivity to entecavir (ETV) or lamivudine[(-)-beta
CC   -2'-deoxy-3'-thiacytidine] (LMV or 3TC). The variant of the invention
CC   demonstrates virucide, antiinflammatory and hepatotropic activities and
CC   may be useful for treating and monitoring nucleoside analogue-resistant
CC   HBV infections, in screening for therapeutic agents or in the rational
CC   design of such agents, as well as in the design of vaccines. The current
CC   sequence is that of the HBV envelope gene protein (HBsAg; Hepatitis B
CC   surface antigen) of the invention which was isolated from patient B
CC   during ETV therapy.
XX
SQ   Sequence 226 AA;

  Query Match             96.1%;  Score 1043;  DB 7;  Length 226;
  Best Local Similarity   95.2%;  Pred. No. 1.2e-86;
  Matches  180;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGTCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| :|||||||||||||| :|||||||||||||||||||
Db        153 PSSWAPGKFLWEWASARFSWLSLVVPFVQWFVGLSPTVWLSFMWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 9
ADG76900
ID   ADG76900 standard; protein; 226 AA.
XX
AC   ADG76900;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Hepatitis B virus envelope amino acid sequence SeqID23.
XX
KW   hepatitis B virus; HBV; polymerase; ADV; LMV; TFV; FTC; ADV; LMV; ADV;
KW   TFV; anti-HBV agent; hepatotropic; virucide; antiinflammatory;
KW   HBV variant polymerase-antagonist; gene therapy; viral component;
KW   inhibiting infection; virus replication; virus release; envelope.
XX
OS   Hepatitis B virus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1. .226
FT                   /label= OTHER
FT                   /note= "OTHER= Any Xaa's in this sequence can be any
FT                   amino acid"
XX
PN   WO2003087351-A1.
XX
PD   23-OCT-2003.
XX
PF   11-APR-2003; 2003WO-AU000432.
```

XX
PR 12-APR-2002; 2002AU-00001710.
PR 26-JUN-2002; 2002AU-00003224.
XX
PA (MELB-) MELBOURNE HEALTH.
PA (AUST-) AUSTIN & REPATRIATION MEDICAL CENT.
PA (SHEA-) SOUTHERN HEALTH.
XX
PI Bartholomeusz AI, Locarnini SA, Ayres A, Colledge D, Sasadeusz J;
PI Tillmann H, Angus PW, Sievert W;
XX
DR WPI; 2003-845324/78.
XX
PT New isolated hepatitis B viral variants with reduced susceptibility to
PT nucleoside analogs, useful for screening, designing and/or developing
PT agents capable of inhibiting infection, replication and/or release of the
PT virus.
XX
PS Example 5; SEQ ID NO 23; 268pp; English.
XX
CC This invention relates to a novel isolated hepatitis B virus (HBV)
CC variant which comprises a nucleoside mutation in a gene encoding a DNA
CC polymerase resulting in at least one amino acid addition, substitution
CC and/or deletion to the polymerase, and exhibiting decreased sensitivity
CC to (for example) ADV, LMV, TFV, or FTC, or ADV and LMV, ADV and TFV,
CC and/or other nucleoside, analogues, anti-HBV agents or their
CC combinations. The invention may be useful for the development of
CC compounds with a hepatotropic, virucide or antiinflammatory activity as
CC HBV variant polymerase-antagonists. In addition, the sequences may be
CC useful for gene therapy. The HBV variants or their component are useful
CC in the rational design of an anti-HBV agent comprising microarray
CC analysis and is based on the crystal structure or NMR structure of a
CC viral component. The methods and compositions of the present invention
CC are also useful for screening, designing and/or developing agents capable
CC of inhibiting infection, replication and/or release of the virus.
XX
SQ Sequence 226 AA;

Query Match 95.9%; Score 1041; DB 7; Length 226;
Best Local Similarity 95.8%; Pred. No. 1.9e-86;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||||| ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSAGXCRTCTTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||| ||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSXLSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221
```

RESULT 10
AAE19897
ID AAE19897 standard; protein; 226 AA.
XX
AC AAE19897;
XX
DT 18-JUN-2002 (first entry)
XX
DE Hepatitis B virus S antigen (HBsAg) sequence.
XX
KW Hepatitis B virus; HBV; infection; virucide; fungicide; antibacterial;
KW cytostatic; immunostimulant; vaccine; ribavirin; immune response; cancer.
XX
OS Hepatitis B virus.
XX
PN WO200213855-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-IB001808.
XX
PR 17-AUG-2000; 2000US-0225767P.
PR 29-AUG-2000; 2000US-0229175P.
PR 03-NOV-2000; 2000US-00705547.
XX
PA (TRIP-) TRIPEP AB.
XX
PI Sallberg M, Hultgren C;
XX
DR WPI; 2002-241837/29.
XX
PT Vaccine compositions for treating and preventing disease, preferably
PT hepatitis C virus infection, comprises ribavirin and antigen that has
PT epitope present in hepatitis C virus.
XX
PS Claim 11; Page 81; 120pp; English.
XX
CC The invention relates to a composition comprising ribavirin and an
CC antigen preferably non structural 3 protein (NS3)/4A fragment of
CC hepatitis C virus (HCV) genome or a peptide or nucleic acid of HCV
CC sequence. The composition is useful for enhancing an immune response to a
CC hepatitis C antigen in humans, domestic, sport or pet species and as
CC vaccines for treating and preventing HCV infections. The composition is
CC also useful for treating viral, bacterial, fungal diseases and cancer.
CC The present sequence is Hepatitis B virus S antigen (HBsAg) sequence
XX
SQ Sequence 226 AA;

Query Match 95.9%; Score 1040; DB 5; Length 226;
Best Local Similarity 95.8%; Pred. No. 2.3e-86;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||| ||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221
```

RESULT 11
ABW00348
ID ABW00348 standard; protein; 226 AA.
XX
AC ABW00348;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis B virus S antigen (HBsAg).
XX
KW Ribavirin; vaccine; immune response; infection; therapy; immunostimulant;
KW virucide.
XX
OS Hepatitis B virus.
XX
PN US2002136740-A1.
XX
PD 26-SEP-2002.

XX
PF 15-AUG-2001; 2001US-00929955.
XX
PR 17-AUG-2000; 2000US-0225767P.
PR 29-AUG-2000; 2000US-0229175P.
XX
PA (SALL/) SALLBERG M.
PA (HULT/) HULTGREN C.
XX
PI Sallberg M, Hultgren C;
XX
DR WPI; 2003-764978/72.
XX
PT Vaccine compositions for treating and preventing disease, preferably
PT hepatitis C virus infection, comprises ribavirin and antigen that has
PT epitope present in hepatitis C virus.
XX
PS Claim 11; Page 44; 0pp; English.
XX
CC The invention relates to a composition comprising ribavirin and an
CC antigen, where the antigen is derived from a hepatitis virus. The vaccine
CC is useful in enhancing the immune response to a hepatitis C antigen where
CC the composition is delivered to an animal identified as requiring an
CC enhanced immune response. The vaccine is useful in the treatment and
CC prevention of hepatitis C infection. The present sequence is Hepatitis B
CC virus S antigen (HBsAg)
XX
SQ Sequence 226 AA;

Query Match 95.9%; Score 1040; DB 7; Length 226;
Best Local Similarity 95.8%; Pred. No. 2.3e-86;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
Db 33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy 61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
Db 93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy 121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
Db 153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy 181 SPLLPIFFC 189
Db 213 LPLLPIFFC 221

RESULT 12
AAY52545
ID AAY52545 standard; protein; 249 AA.
XX
AC AAY52545;
XX
DT 06-AUG-2003 (revised)
DT 28-FEB-2000 (first entry)
XX
DE Pan DR epitope/HBV surface antigen fusion protein.
XX
KW Chimeric; HBV; surface antigen; pan DR epitope; expression vector;
KW promoter; major histocompatibility complex; MHC; targetting; peptide;
KW epitope; antigen; presentation; class I; cytosolic pathway;
KW endoplasmic reticulum; class II; extracellular antigen;
KW endocytic pathway; helper T lymphocyte; HTL; universal epitope;
KW cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;
KW vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;
KW autoimmune disease; activation; antiviral; antimalarial;
KW immunoprotective.
XX
OS Synthetic.

OS Hepatitis B virus.
XX
PN WO9958658-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US010646.
XX
PR 13-MAY-1998; 98US-00078904.
PR 15-MAY-1998; 98US-0085751P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
PI Chesnut RW;
XX
DR WPI; 2000-039103/03.
DR N-PSDB; AAZ38623.
XX
PT Expression vectors encoding major histocompatibility targeting sequence,
PT used as, e.g. tumor vaccines.
XX
PS Example 1; Fig 8; 130pp; English.
XX
CC This sequence represents the fusion protein encoded by a pan DR
CC epitope/HBV surface antigen fusion gene, PADRE-HBV-s, used in an
CC exemplification of the present invention. The invention relates to a
CC novel expression vector comprising a promoter operably linked to a fusion
CC gene encoding a major histocompatibility complex (MHC) targetting
CC sequence, and two or more heterologous peptide epitopes. The MHC
CC targetting sequence may be a class I targetting sequence, which directs
CC an MHC class I epitope to a cytosolic pathway or to the endoplasmic
CC reticulum, or an MHC class II targetting sequence, which directs
CC extracellular antigens to enter the endocytic pathway to be processed
CC into antigen peptides for presentation on MHC class II molecules. The
CC heterologous epitopes may comprise either helper T lymphocyte (HTL)
CC epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
CC epitope such as a pan DR epitope (PADRE). The vectors are useful for
CC stimulating an immune response in vivo, as well as for use in assaying
CC the human immunogenicity of a human T cell peptide epitope in vivo in a
CC non-human mammal. They provide a nucleic acid vaccine for enhancing
CC immunity against infectious pathogens, such as viruses (e.g., HIV,
CC hepatitis B (HBV and hepatitis C (HCV)) bacteria, protozoa (e.g.,
CC Plasmodium falciparum, the cause of malaria) and also tumour cells and
CC autoimmune diseases. Universal MHC class II epitopes are advantageously
CC combined with other MHC class I and class II epitopes to increase the
CC number of cells that are activated in response to a given antigen and
CC provide a broader population coverage of MHC-reactive alleles. (Updated
CC on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 249 AA;

Query Match 95.9%; Score 1040; DB 3; Length 249;
Best Local Similarity 95.8%; Pred. No. 2.5e-86;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
Db 56 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 115

Qy 61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
Db 116 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 175

Qy 121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
Db 176 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 235

Qy 181 SPLLPIFFC 189
Db 236 LPLLPIFFC 244

```
RESULT 13
AAR27471
ID   AAR27471 standard; protein; 281 AA.
XX
AC   AAR27471;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1993  (first entry)
XX
DE   spsAg protein.
XX
KW   Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
KW   vaccinia virus; H6; early/late; promoter; NYVAC; recombinant; HBV L;
KW   large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core; S1;
KW   S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
KW   deletion loci; recipient loci.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .55
FT                   /label= S2
FT   Region          56. .281
FT                   /label= S
XX
PN   WO9215672-A1.
XX
PD   17-SEP-1992.
XX
PF   09-MAR-1992;   92WO-US001906.
XX
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   06-MAR-1992;   92US-00847951.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Perkus ME,  Taylor J,  Tartaglia J,  Norton EK;
PI   Riviere M,  De Taisne C,  Limbach KJ,  Johnson GP,  Pincus SE,  Cox WI;
PI   Francis J,  Gettig RR;
XX
DR   WPI; 1992-331718/40.
DR   N-PSDB; AAQ29103.
XX
PT   Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
PT   against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
PT   mumps etc.
XX
PS   Disclosure; Fig 9; 456pp; English.
XX
CC   The sequence given is encoded by an expression cassette which consists of
CC   the hepatitis B virus (HBV) M protein (small pre-S antigen, spsAg) gene
CC   precisely linked to a modified synthetic vaccinia virus H6 early/late
CC   promoter. This DNA sequence was used in the construction of a NYVAC
CC   recombinant expressing the HBV gene. Other HBV genes were also used in
CC   the construction. These were HBV L (large pre-S antigen, lpsAg) and a
CC   fusion protein composed of the entire pre-S region (S12/core, S1 + S2).
CC   Each of these gene sequences were inserted individually into three
CC   different sites of NYVAC separated by from each other by large regions of
CC   vaccinia DNA containing essential genes. NYVAC is a Copenhagen vaccine
CC   strain of vaccinia virus which has been modified by deletion of six non-
CC   essential regions of the genome encoding known or potential virulence
CC   factors. The deletion loci were engineered as recipient loci for the
CC   insertion of foreign genes. The spacing of the three inserted sequences
CC   ensured that any recombination that did occur would lead to disruption of
CC   the vaccinia genome and would cause unviable vaccinia virus. See also
CC   AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 281 AA;

  Query Match             95.9%;  Score 1040;  DB 2;  Length 281;
  Best Local Similarity   95.8%;  Pred. No. 2.9e-86;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 14
AAY32835
ID   AAY32835 standard; protein; 281 AA.
XX
AC   AAY32835;
XX
DT   27-AUG-2003  (revised)
DT   29-OCT-1999  (first entry)
XX
DE   HBsAg PreS2-S region protein sequence.
XX
KW   HBsAg; PreS2-S; recombinant antigen library; disease-related antigen;
KW   multivalent antigenic polypeptide production; infection; allergen;
KW   asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy;
KW   multiple sclerosis; inflammatory condition; cancer; contraception;
KW   immune response; hepatitis b surface antigen.
XX
OS   Hepatitis B virus.
XX
PN   WO9941383-A1.
XX
PD   19-AUG-1999.
XX
PF   10-FEB-1999;   99WO-US002944.
XX
PR   11-FEB-1998;   98US-00021769.
PR   11-FEB-1998;   98US-0074294P.
PR   23-OCT-1998;   98US-0105509P.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Punnonen J,  Bass SH,  Whalen RG,  Howard R,  Stemmer WPC;
XX
DR   WPI; 1999-518452/43.
DR   N-PSDB; AAZ10968.
XX
PT   Recombinant multivalent antigenic polypeptide produced by recombining
PT   nucleic acid sequences and screening, used in vaccines against e.g.
PT   infections and cancer.
XX
PS   Example 14; Fig 17; 153pp; English.
XX
CC   This sequence is the hepatitis B virus (HBV) surface antigen (HBsAg)
CC   PreS2-S region. This sequence was used to create a recombinant antigen
CC   library. The library comprises recombinant nucleic acids encoding
CC   antigenic polypeptides and is produced by recombination of at least two
CC   forms of nucleic acid, differing by at least two nucleotides, encoding a
CC   disease-related antigenic polypeptide. The library can be used to produce
CC   a recombinant multivalent antigenic polypeptides of the invention, that
CC   contains at least two antigenic determinants (AD) from different
CC   polypeptides. The multivalent antigenic polypeptides are used in vaccines
CC   to induce a protective or therapeutic response to a wide variety of
CC   infectious agents (bacteria, viruses, parasites, including Plasmodium
CC   falciparum); allergens; asthma; autoimmune disease (e.g. rheumatoid
CC   arthritis, diabetes, multiple sclerosis); other inflammatory conditions
```

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CC   and cancer, also, where directed against sperm antigens,they can be used
CC   for contraception. The multivalent peptides can be evolved to induce an
CC   optimised immune response against a wide variety of antigens,
CC   particularly a broad spectrum response to many different strains of a
CC   pathogen, including strains that are likely to appear in the future.
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 281 AA;

  Query Match             95.9%;  Score 1040;  DB 2;  Length 281;
  Best Local Similarity   95.8%;  Pred. No. 2.9e-86;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 15
ADG76901
ID   ADG76901 standard; protein; 309 AA.
XX
AC   ADG76901;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Hepatitis B virus envelope amino acid sequence SeqID24.
XX
KW   hepatitis B virus; HBV; polymerase; ADV; LMV; TFV; FTC; ADV; LMV; ADV;
KW   TFV; anti-HBV agent; hepatotropic; virucide; antiinflammatory;
KW   HBV variant polymerase-antagonist; gene therapy; viral component;
KW   inhibiting infection; virus replication; virus release; envelope.
XX
OS   Hepatitis B virus.
XX
PN   WO2003087351-A1.
XX
PD   23-OCT-2003.
XX
PF   11-APR-2003; 2003WO-AU000432.
XX
PR   12-APR-2002; 2002AU-00001710.
PR   26-JUN-2002; 2002AU-00003224.
XX
PA   (MELB-) MELBOURNE HEALTH.
PA   (AUST-) AUSTIN & REPATRIATION MEDICAL CENT.
PA   (SHEA-) SOUTHERN HEALTH.
XX
PI   Bartholomeusz AI,  Locarnini SA,  Ayres A,  Colledge D,  Sasadeusz J;
PI   Tillmann H,  Angus PW,  Sievert W;
XX
DR   WPI; 2003-845324/78.
XX
PT   New isolated hepatitis B viral variants with reduced susceptibility to
PT   nucleoside analogs, useful for screening, designing and/or developing
PT   agents capable of inhibiting infection, replication and/or release of the
PT   virus.
XX
PS   Example 5; SEQ ID NO 24; 268pp; English.
XX
CC   This invention relates to a novel isolated hepatitis B virus (HBV)
CC   variant which comprises a nucleoside mutation in a gene encoding a DNA
CC   polymerase resulting in at least one amino acid addition, substitution
CC   and/or deletion to the polymerase, and exhibiting decreased sensitivity
CC   to (for example) ADV, LMV, TFV, or FTC, or ADV and LMV, ADV and TFV,
CC   and/or other nucleoside, analogues, anti-HBV agents or their
CC   combinations. The invention may be useful for the development of
CC   compounds with a hepatotropic, virucide or antiinflammatory activity as
CC   HBV variant polymerase-antagonists. In addition, the sequences may be
CC   useful for gene therapy. The HBV variants or their component are useful
CC   in the rational design of an anti-HBV agent comprising microarray
CC   analysis and is based on the crystal structure or NMR structure of a
CC   viral component. The methods and compositions of the present invention
CC   are also useful for screening, designing and/or developing agents capable
CC   of inhibiting infection, replication and/or release of the virus.
XX
SQ   Sequence 309 AA;

  Query Match             95.9%;  Score 1040;  DB 7;  Length 309;
  Best Local Similarity   95.8%;  Pred. No. 3.2e-86;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 175

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        176 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 235

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        236 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 295

Qy        181 SPLLPIFFC 189
              |||||||||
Db        296 LPLLPIFFC 304


Search completed: July 25, 2005, 11:21:29
Job time : 166 secs
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GenCore version 5.1.6

)M protein - protein search, using sw model

Run on: July 25, 2005, 11:13:41 ; Search time 39 Seconds
(without alignments)
466.281 Million cell updates/sec

Title: US-09-823-077C-7
Perfect score: 1085
Sequence: 1 DSWWTSLNFLGGTTVCLGQN.....GPSLYSILSPFSPLLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1054	97.1	226	1	JQ1571	major surface anti
2	1054	97.1	389	1	SAVLBH	large surface anti
3	1054	97.1	389	2	S20745	surface antigen -
4	1054	97.1	389	2	S20753	surface antigen -
5	1050	96.8	226	2	JQ2077	surface antigen -
6	1050	96.8	226	2	JQ2076	surface antigen -
7	1049	96.7	226	2	JQ2078	surface antigen -
8	1047	96.5	226	2	JQ2079	surface antigen -
9	1046	96.4	226	2	JQ2075	surface antigen -
10	1046	96.4	226	2	JQ2073	surface antigen -
11	1046	96.4	389	2	S32202	large surface anti
12	1044	96.2	226	2	JQ2069	surface antigen -
13	1043	96.1	226	2	JQ2081	surface antigen -
14	1041	95.9	389	2	S47407	surface antigen -
15	1040	95.9	226	1	JQ1572	major surface anti
16	1040	95.9	226	2	JQ2065	surface antigen -
17	1040	95.9	226	2	JQ2067	surface antigen -
18	1040	95.9	226	2	JQ2083	surface antigen -
19	1040	95.9	389	1	SAVLAH	large surface anti
20	1037	95.6	226	2	JQ2066	surface antigen -
21	1037	95.6	226	2	JQ2063	surface antigen -
22	1037	95.6	389	1	SAVLA1	large surface anti
23	1037	95.6	389	1	SAVLAJ	large surface anti
24	1036	95.5	226	2	JQ2068	surface antigen -
25	1031	95.0	226	2	JQ2070	surface antigen -
26	1030	94.9	226	2	JQ2080	surface antigen -
27	1027	94.7	226	2	JQ2072	surface antigen -
28	1017	93.7	226	2	JQ2050	surface antigen -
29	1016	93.6	226	2	JQ2092	surface antigen -
30	1012	93.3	226	2	JQ2085	surface antigen -
31	1010	93.1	226	2	JQ2054	surface antigen -
32	1007	92.8	226	1	JQ1573	major surface anti
33	1007	92.8	226	2	JQ2052	surface antigen -
34	1007	92.8	226	2	JQ2055	surface antigen -
35	1007	92.8	226	2	JQ2045	surface antigen -
36	1007	92.8	389	2	S41871	surface antigen -
37	1007	92.8	400	1	JQ1575	major surface anti
38	1007	92.8	400	1	SAVLVD	large surface anti
39	1006	92.7	226	2	JQ2087	surface antigen -
40	1006	92.7	226	2	JQ2089	surface antigen -
41	1006	92.7	226	2	JQ2090	surface antigen -
42	1006	92.7	226	2	JQ2091	surface antigen -
43	1005	92.6	226	1	JQ1577	major surface anti
44	1005	92.6	226	1	JQ1578	major surface anti
45	1004	92.5	226	1	SAVLHV	major surface anti

ALIGNMENTS

RESULT 1
JQ1571
major surface antigen - hepatitis B virus (subtype ayw2)
C;Species: hepatitis B virus, HBV
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JQ1571; JQ2074
R;Norder, H.; Hammas, B.; Loefdahl, S.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
A;Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis
A;Reference number: JQ1570; MUID:92268879; PMID:1588323
A;Accession: JQ1571
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q69601; GB:X75662; NID:g416086; PIDN:CAA53349.1; PID:g416087
A;Experimental source: subtype ayw2, strain P2
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2074
A;Molecule type: DNA
A;Residues: 1-226 <NO2>
A;Experimental source: subtype ayw2, strain Ren
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.1%; Score 1054; DB 1; Length 226;
Best Local Similarity 96.8%; Pred. No. 2.5e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221
```

RESULT 2
SAVLBH
large surface antigen - hepatitis B virus (subtype ayw, strain pHB320)
N;Contains: major surface antigen; middle surface antigen
C;Species: hepatitis B virus, HBV
A;Note: host Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A03704; PQ0585
R;Bichko, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985
A;Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A;Reference number: A05237; MUID:85204397; PMID:3996597
A;Accession: A03704
A;Molecule type: DNA
A;Residues: 1-389 <BIC>
A;Cross-references: UNIPROT:Q9WJC4; GB:X02496; NID:g62280; PIDN:CAB41701.1; PID:g4704321
R;Norder, H.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A;Title: Molecular basis of hepatitis B virus serotype variations within the four major
A;Reference number: PQ0453; MUID:93107848; PMID:1469353
A;Accession: PQ0585
A;Molecule type: DNA
A;Residues: 264-343 <NOR>
A;Experimental source: subtype ayw2, Tav
C;Genetics:
A;Gene: pre-S1/pre-S2/S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F;164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F;4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.1%; Score 1054; DB 1; Length 389;
Best Local Similarity 96.8%; Pred. No. 3.8e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384
```

RESULT 3
S20745
surface antigen - hepatitis B virus (subtype ayw, patient C)
N;Alternate names: HBs antigen
N;Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient C
C;Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S20745
R;Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati
A;Reference number: S20745
A;Accession: S20745
A;Molecule type: DNA
A;Residues: 1-389 <LAI>
A;Cross-references: UNIPROT:Q67871; EMBL:X65257; NID:g59429; PIDN:CAA46349.1; PID:g59430
A;Experimental source: subtype ayw, patient C
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen
F;1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS
F;1-108/Domain: pre-S1 domain #status predicted <PRE1>
F;109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted
F;109-163/Domain: pre-S2 domain #status predicted <PRE2>
F;164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 97.1%; Score 1054; DB 2; Length 389;
Best Local Similarity 96.8%; Pred. No. 3.8e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384
```

RESULT 4
S20753
surface antigen - hepatitis B virus (subtype ayw, patient E)
N;Alternate names: envelope protein; HBs antigen
N;Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mi
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient E
C;Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S20753
R;Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negat
A;Reference number: S20745
A;Accession: S20753
A;Molecule type: DNA
A;Residues: 1-389 <LAI>
A;Cross-references: UNIPROT:Q67879; EMBL:X65259; NID:g59439; PIDN:CAA46357.1; PID:g5944
A;Experimental source: subtype ayw, patient E
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen
F;1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1
F;1-108/Domain: pre-S1 domain #status predicted <PRE1>
F;109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <
F;109-163/Domain: pre-S2 domain #status predicted <PRE2>
F;164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 97.1%; Score 1054; DB 2; Length 389;
Best Local Similarity 96.8%; Pred. No. 3.8e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375
```

```
Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 5
JQ2077
surface antigen - hepatitis B virus (subtype ayw2, strain Ben)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2077
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2077
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q9WNS1; UNIPROT:Q9QAF8; UNIPROT:Q8JXA1; UNIPROT:Q69601; UNIP
PROT:Q9WHR7; UNIPROT:Q9YTI5; UNIPROT:Q9IP39; UNIPROT:Q9Q3E2; UNIPROT:Q9E6U0; UNIPROT:Q9W
PX80; UNIPROT:Q67917; UNIPROT:Q9QAG3; UNIPROT:Q998M0; UNIPROT:Q69600; UNIPROT:Q8BAP4; UN
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.8%;  Score 1050;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 5.2e-77;
  Matches  182;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||:|||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWIMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 6
JQ2076
surface antigen - hepatitis B virus (subtype ayw2, strain Hac)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2076
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2076
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q9WNS1; UNIPROT:Q9QAF8; UNIPROT:Q8JXA1; UNIPROT:Q69601; UNIP
PROT:Q9WHR7; UNIPROT:Q9YTI5; UNIPROT:Q9IP39; UNIPROT:Q9Q3E2; UNIPROT:Q9E6U0; UNIPROT:Q9W
PX80; UNIPROT:Q67917; UNIPROT:Q9QAG3; UNIPROT:Q998M0; UNIPROT:Q69600; UNIPROT:Q8BAP4; UN
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.8%;  Score 1050;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 5.2e-77;
  Matches  182;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGNSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 7
JQ2078
surface antigen - hepatitis B virus (subtype ayw, strain aywmut)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2078
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2078
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q67886
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.7%;  Score 1049;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 6.3e-77;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGNSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 8
JQ2079
surface antigen - hepatitis B virus (subtype ayw2, strain 7794/85)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2079
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2079
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
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A;Cross-references: UNIPROT:Q9E6U1; UNIPROT:Q9WHR7; UNIPROT:Q9YTI5; UNIPROT:Q9IF39; UNIP
PROT:Q91T77; UNIPROT:Q9QAW7; UNIPROT:O72527; UNIPROT:Q9IZS1; UNIPROT:O72528; UNIPROT:Q9Y
QAG3; UNIPROT:Q998M0; UNIPROT:Q69600; UNIPROT:Q8BAP4; UNIPROT:Q69591; UNIPROT:Q9PWW6; UN
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.5%;  Score 1047;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 9.1e-77;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||||:|||||||||||||| |||||||| ||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFDGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 IPLLPIFFC 221


RESULT 9
JQ2075
surface antigen - hepatitis B virus (subtype ayw2, strain pPYW310)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2075
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2075
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q8BAP4
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.4%;  Score 1046;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 1.1e-76;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCAGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||||:|||||||||||||| |||||||| ||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 10
JQ2073
surface antigen - hepatitis B virus (subtype ayw3, strain 727/92)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2073
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2073
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q67917
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.4%;  Score 1046;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 1.1e-76;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||||| ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSAGPCRTCTTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 11
S32202
large surface antigen - hepatitis B virus (subtype ayw, isolate patient C1005)
N;Contains: major surface antigen; middle surface antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, isolate patient C1005
C;Date: 20-Feb-1995 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C;Accession: S32202
R;Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
A;Description: Identification and sequence analysis of hepatitis B virus DNA in immunolo
A;Reference number: S32202
A;Accession: S32202
A;Molecule type: DNA
A;Residues: 1-389 <PRE>
A;Cross-references: UNIPROT:Q67920; EMBL:X72702
A;Experimental source: subtype ayw, isolate patient C1005
C;Genetics:
A;Gene: pre-S1/pre-S2/S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen
F;1-389/Product: large surface antigen (gene pre-S1/pre-S2/S) #status predicted <DSL>
F;109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F;164-389/Product: major surface antigen (gene S) #status predicted <MSA>

  Query Match             96.4%;  Score 1046;  DB 2;  Length 389;
  Best Local Similarity   96.3%;  Pred. No. 1.7e-76;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||||| ||||||||||||||||||||||||||
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Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSAGPCRTCTTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 12
JQ2069
surface antigen - hepatitis B virus (subtype ayw4, strain 17798/73)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2069
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2069
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:O91939; UNIPROT:Q9J1J8; UNIPROT:Q91T65; UNIPROT:Q91T89; UNIP
PROT:Q9IF39; UNIPROT:Q91T90; UNIPROT:Q9Q3E2; UNIPROT:Q9E6U0; UNIPROT:Q9WHR9; UNIPROT:Q9Q
PX80; UNIPROT:Q67917; UNIPROT:Q9QAG3; UNIPROT:Q998M0; UNIPROT:Q69600; UNIPROT:Q8BAP4; UN
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.2%;  Score 1044;  DB 2;  Length 226;
  Best Local Similarity   96.3%;  Pred. No. 1.6e-76;
  Matches  182;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||||| ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTIAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 13
JQ2081
surface antigen - hepatitis B virus (subtype ayw2, strain pHBV138)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2081
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2081
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q8QXQ3; UNIPROT:Q89627; UNIPROT:Q8QXP8; UNIPROT:O56569; UNIP
PROT:Q67915; UNIPROT:Q8JN14; UNIPROT:Q9Q3D9; UNIPROT:Q9WHR7; UNIPROT:Q9YTI5; UNIPROT:Q9I
PX80; UNIPROT:Q67917; UNIPROT:Q9QAG3; UNIPROT:Q998M0; UNIPROT:Q69600; UNIPROT:Q8BAP4; UN
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen

  Query Match             96.1%;  Score 1043;  DB 2;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 1.9e-76;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPISNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||||| ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGSCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPIVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 14
S47407
surface antigen - hepatitis B virus (subtype ayw4)
N;Alternate names: envelope protein; HBs antigen
N;Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw4
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S47407; JQ2071
R;Pluciennicczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolat
A;Reference number: S47404
A;Accession: S47407
A;Molecule type: DNA
A;Residues: 1-389 <PLU>
A;Cross-references: UNIPROT:Q67893; EMBL:Z35716; NID:g527435; PIDN:CAA84788.1; PID:g5274
A;Experimental source: subtype ayw4
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup D
A;Accession: JQ2071
A;Molecule type: DNA
A;Residues: 164-389 <NOR>
A;Experimental source: subtype ayw3, strain 8950/90
C;Genetics:
A;Gene: S
A;Introns: 111/3
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: surface antigen
F;1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F;1-108/Domain: pre-S1 domain #status predicted <PRE1>
F;109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <P
F;109-163/Domain: pre-S2 domain #status predicted <PRE2>
F;164-389/Product: surface antigen S (small envelope protein) #status predicted <SAG>

  Query Match             95.9%;  Score 1041;  DB 2;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 4.2e-76;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||||| ||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSVGPCRTCTTTVQGTSMYPSCCCTKPSDGNCTCIPI 315
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Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
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Db        316 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
                |||||||
Db        376 LPLLPIFFC 384


RESULT 15
JQ1572
major surface antigen - hepatitis B virus (subtype ayw3, strain P3)
C;Species: hepatitis B virus, HBV
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JQ1572
R;Norder, H.; Hammas, B.; Loefdahl, S.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
A;Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis
A;Reference number: JQ1570; MUID:92268879; PMID:1588323
A;Accession: JQ1572
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q8QXP8; UNIPROT:O56569; UNIPROT:Q67879; UNIPROT:Q998M1; UNIP
PROT:Q8JN14; UNIPROT:Q9Q3D9; UNIPROT:Q9WHR7; UNIPROT:Q9YTI5; UNIPROT:Q9IF39; UNIPROT:Q9Q
PX80; UNIPROT:Q67917; UNIPROT:Q9QAG3; UNIPROT:Q998M0; UNIPROT:Q69600; UNIPROT:Q8BAP4; UN
C;Genetics:
A;Gene: S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;3/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             95.9%;  Score 1040;  DB 1;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 3.3e-76;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
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Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
                |||||||
Db        213 LPLLPIFFC 221


Search completed: July 25, 2005, 11:25:13
Job time : 39 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 25, 2005, 11:15:11 ; Search time 42 Seconds
(without alignments)
335.921 Million cell updates/sec

Title: US-09-823-077C-7
Perfect score: 1085
Sequence: 1 DSWWTSLNFLGGTTVCLGQN.....GPSLYSILSPFSPLLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1040	95.9	226	4	US-10-104-966-10	Sequence 10, Appl
2	1040	95.9	249	4	US-09-311-784A-16	Sequence 16, Appl
3	1040	95.9	281	1	US-08-105-483-214	Sequence 214, App
4	1040	95.9	281	1	US-08-709-209-214	Sequence 214, App
5	1040	95.9	281	1	US-08-458-101-214	Sequence 214, App
6	1040	95.9	281	4	US-09-247-890-12	Sequence 12, Appl
7	1040	95.9	281	4	US-09-724-969-12	Sequence 12, Appl
8	1040	95.9	281	4	US-09-724-852-12	Sequence 12, Appl
9	1040	95.9	389	1	US-08-105-483-216	Sequence 216, App
10	1040	95.9	389	1	US-08-105-483-219	Sequence 219, App
11	1040	95.9	389	1	US-08-709-209-216	Sequence 216, App
12	1040	95.9	389	1	US-08-709-209-219	Sequence 219, App
13	1040	95.9	389	1	US-08-458-101-216	Sequence 216, App
14	1040	95.9	389	1	US-08-458-101-219	Sequence 219, App
15	1040	95.9	389	3	US-08-486-099-106	Sequence 106, App
16	1040	95.9	389	3	US-08-360-107A-116	Sequence 116, App
17	1040	95.9	389	3	US-08-484-223B-106	Sequence 106, App
18	1040	95.9	389	3	US-08-919-597-106	Sequence 106, App
19	1040	95.9	389	3	US-08-475-668A-106	Sequence 106, App
20	1040	95.9	389	3	US-08-485-551A-106	Sequence 106, App
21	1040	95.9	389	3	US-08-471-913A-106	Sequence 106, App
22	1040	95.9	389	3	US-08-485-264A-106	Sequence 106, App
23	1040	95.9	389	3	US-08-474-349A-106	Sequence 106, App
24	1040	95.9	389	4	US-08-470-896-106	Sequence 106, App
25	1040	95.9	389	4	US-08-485-546A-106	Sequence 106, App
26	1040	95.9	389	4	US-08-487-266A-106	Sequence 106, App
27	1040	95.9	397	5	PCT-US96-10602-6	Sequence 6, Appli
28	1033	95.2	226	5	PCT-US96-10602-14	Sequence 14, Appl
29	1007	92.8	225	6	5436139-4	Patent No. 5436139
30	1007	92.8	225	6	5436139-4	Patent No. 5436139
31	1007	92.8	226	6	5196194-21	Patent No. 5196194
32	1007	92.8	226	6	5436139-5	Patent No. 5436139
33	1007	92.8	226	6	5196194-21	Patent No. 5196194
34	1007	92.8	226	6	5436139-5	Patent No. 5436139
35	1007	92.8	281	4	US-09-721-480-3	Sequence 3, Appli
36	1007	92.8	390	4	US-09-721-480-5	Sequence 5, Appli
37	1007	92.8	531	4	US-09-721-480-7	Sequence 7, Appli
38	1004	92.5	387	4	US-09-350-841A-1592	Sequence 1592, Ap
39	1004	92.5	423	2	US-08-760-797A-1	Sequence 1, Appli
40	1004	92.5	424	2	US-08-760-797A-3	Sequence 3, Appli
41	1004	92.5	424	3	US-08-932-929B-1	Sequence 1, Appli
42	1004	92.5	424	3	US-08-932-929B-3	Sequence 3, Appli
43	995.5	91.8	395	6	5196194-18	Patent No. 5196194
44	995.5	91.8	395	6	5196194-18	Patent No. 5196194
45	992	91.4	226	1	US-08-378-011A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-104-966-10
; Sequence 10, Application US/10104966
; Patent No. 6680059
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: TRIPEP.23AUSC1
; CURRENT APPLICATION NUMBER: US/10/104,966
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-10-104-966-10

Query Match 95.9%; Score 1040; DB 4; Length 226;
Best Local Similarity 95.8%; Pred. No. 7.7e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        153 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221
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RESULT 2
US-09-311-784A-16
; Sequence 16, Application US/09311784A

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; Patent No. 6534482
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/09/311,784A
;  CURRENT FILING DATE:  1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-HBV-s
US-09-311-784A-16

  Query Match             95.9%;  Score 1040;  DB 4;  Length 249;
  Best Local Similarity   95.8%;  Pred. No. 8.6e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||
Db        116 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 175

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        176 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 235

Qy        181 SPLLPIFFC 189
              |||||||||
Db        236 LPLLPIFFC 244


RESULT 3
US-08-105-483-214
; Sequence 214, Application US/08105483
; Patent No. 5494807
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/105,483
;      FILING DATE:  12-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  214:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  281 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-105-483-214

  Query Match             95.9%;  Score 1040;  DB 1;  Length 281;
  Best Local Similarity   95.8%;  Pred. No. 9.8e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
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Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 4
US-08-709-209-214
; Sequence 214, Application US/08709209
; Patent No. 5762938
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,209
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
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;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  214:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  281 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-709-209-214

  Query Match            95.9%;  Score 1040;  DB 1;  Length 281;
  Best Local Similarity  95.8%;  Pred. No. 9.8e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
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Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              |||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 5
US-08-458-101-214
; Sequence 214, Application US/08458101
; Patent No. 5766599
; GENERAL INFORMATION:
;   APPLICANT:  Paoletti, Enzo
;   APPLICANT:  Perkus, Marion E.
;   APPLICANT:  Taylor, Jill
;   APPLICANT:  Tartaglia, James
;   APPLICANT:  No. 5766599ton, Elizabeth K.
;   APPLICANT:  Riviere, Michel
;   APPLICANT:  de Taisne, Charles
;   APPLICANT:  Limbach, Keith J.
;   APPLICANT:  Johnson, Gerard P.
;   APPLICANT:  Pincus, Steven E.
;   APPLICANT:  Cox, William I.
;   APPLICANT:  Audonnet, Jean-Christophe Francis
;   APPLICANT:  Gettig, Russell Robert
;   TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;   TITLE OF INVENTION:  STRAIN
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Curtis, Morris & Safford
;     ADDRESSEE:  c/o William S. Frommer
;     STREET:  530 Fifth Avenue
;     CITY:  New York
;     STATE:  NY
;     COUNTRY:  USA
;     ZIP:  10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/458,101
;     FILING DATE:  01-JUN-1995
;     CLASSIFICATION:  424
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2740
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  214:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  281 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-458-101-214

  Query Match            95.9%;  Score 1040;  DB 1;  Length 281;
  Best Local Similarity  95.8%;  Pred. No. 9.8e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
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Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
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Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 6
US-09-247-890-12
; Sequence 12, Application US/09247890
; Patent No. 6541011
; GENERAL INFORMATION:
;  APPLICANT: Punnonen, Juha
;  APPLICANT: Bass, Steven H.
;  APPLICANT: Whalen, Robert Gerald
;  APPLICANT: Howard, Russell
;  APPLICANT: Stemmer, Willem P.C.
;  APPLICANT: Maxygen, Inc.
;  TITLE OF INVENTION: Antigen Library Immunization
;  FILE REFERENCE: 018097-028710US
;  CURRENT APPLICATION NUMBER: US/09/247,890
;  CURRENT FILING DATE: 1999-02-10
;  EARLIER APPLICATION NUMBER: US 60/074,294
;  EARLIER FILING DATE: 1998-02-11
;  EARLIER APPLICATION NUMBER: US 60/105,509
;  EARLIER FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Hepatitis B virus
US-09-247-890-12

  Query Match            95.9%;  Score 1040;  DB 4;  Length 281;
  Best Local Similarity  95.8%;  Pred. No. 9.8e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207
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Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 7
US-09-724-969-12
; Sequence 12, Application US/09724969
; Patent No. 6569435
; GENERAL INFORMATION:
;  APPLICANT: Punnonen, Juha
;  APPLICANT:  Bass, Steven H.
;  APPLICANT:  Whalen, Robert Gerald
;  APPLICANT:  Howard, Russell
;  APPLICANT:  Stemmer, Willem P.C.
;  APPLICANT:  Maxygen, Inc.
;  TITLE OF INVENTION: Antigen Library Immunization
;  FILE REFERENCE: 018097-028710US
;  CURRENT APPLICATION NUMBER: US/09/724,969
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: 09/247,890
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/105,509
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Hepatitis B virus
US-09-724-969-12

  Query Match             95.9%;  Score 1040;  DB 4;  Length 281;
  Best Local Similarity   95.8%;  Pred. No. 9.8e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 8
US-09-724-852-12
; Sequence 12, Application US/09724852
; Patent No. 6576757
; GENERAL INFORMATION:
;  APPLICANT: Punnonen, Juha
;  APPLICANT:  Bass, Steven H.
;  APPLICANT:  Whalen, Robert Gerald
;  APPLICANT:  Howard, Russell
;  APPLICANT:  Stemmer, Willem P.C.
;  APPLICANT:  Maxygen, Inc.
;  TITLE OF INVENTION: Antigen Library Immunization
;  FILE REFERENCE: 018097-028710US
;  CURRENT APPLICATION NUMBER: US/09/724,852
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US/09/247,890
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Hepatitis B virus
US-09-724-852-12

  Query Match             95.9%;  Score 1040;  DB 4;  Length 281;
  Best Local Similarity   95.8%;  Pred. No. 9.8e-89;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
              |||||||||
Db        268 LPLLPIFFC 276


RESULT 9
US-08-105-483-216
; Sequence 216, Application US/08105483
; Patent No. 5494807
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/105,483
;      FILING DATE:  12-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  216:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-105-483-216

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 10
US-08-105-483-219
; Sequence 219, Application US/08105483
; Patent No. 5494807
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/105,483
;      FILING DATE:  12-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  219:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-105-483-219

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 11
US-08-709-209-216
; Sequence 216, Application US/08709209
; Patent No. 5762938
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,209
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  216:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-709-209-216

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
              |||||||||
Db        376 LPLLPIFFC 384


RESULT 11
US-08-709-209-216
; Sequence 216, Application US/08709209
; Patent No. 5762938
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,209
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  216:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-709-209-216

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNPLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIPLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
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                ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
                ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
                |||||||| |
Db        376 LPLLPIFFC 384


RESULT 12
US-08-709-209-219
; Sequence 219, Application US/08709209
; Patent No. 5762938
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  462
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,209
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  219:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-709-209-219

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 255

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
                ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        256 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 315

Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
                ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        316 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375

Qy        181 SPLLPIFFC 189
                |||||||| |
Db        376 LPLLPIFFC 384


RESULT 13
US-08-458-101-216
; Sequence 216, Application US/08458101
; Patent No. 5766599
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Perkus, Marion E.
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  No. 5766599ton, Elizabeth K.
;    APPLICANT:  Riviere, Michel
;    APPLICANT:  de Taisne, Charles
;    APPLICANT:  Limbach, Keith J.
;    APPLICANT:  Johnson, Gerard P.
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Audonnet, Jean-Christophe Francis
;    APPLICANT:  Gettig, Russell Robert
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,101
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2740
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  216:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-458-101-216

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
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Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
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Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
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Db        376 LPLLPIFFC 384


RESULT 14
US-08-458-101-219
; Sequence 219, Application US/08458101
; Patent No. 5766599
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Perkus, Marion E.
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  No. 5766599ton, Elizabeth K.
;    APPLICANT:  Riviere, Michel
;    APPLICANT:  de Taisne, Charles
;    APPLICANT:  Limbach, Keith J.
;    APPLICANT:  Johnson, Gerard P.
;    APPLICANT:  Pincus, Steven E.
;    APPLICANT:  Cox, William I.
;    APPLICANT:  Audonnet, Jean-Christophe Francis
;    APPLICANT:  Gettig, Russell Robert
;    TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;    TITLE OF INVENTION:  STRAIN
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      ADDRESSEE:  c/o William S. Frommer
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,101
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2740
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  219:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-458-101-219

  Query Match             95.9%;  Score 1040;  DB 1;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
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Qy        181 SPLLPIFFC 189
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Db        376 LPLLPIFFC 384


RESULT 15
US-08-486-099-106
; Sequence 106, Application US/08486099
; Patent No. 6013263
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF
;    TITLE OF INVENTION:  MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
;    TITLE OF INVENTION:  B VIRUS TRANSMISSION
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,099
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  106:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-486-099-106

  Query Match             95.9%;  Score 1040;  DB 3;  Length 389;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-88;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
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Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              |||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
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Qy        121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
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Db        316 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 375
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Title: US-09-823-077C-7
Perfect score: 1085
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1046	96.4	389	14	US-10-169-668-6	Sequence 6, Appli
3	1043	96.1	226	18	US-10-911-464B-36	Sequence 36, Appl
4	1040	95.9	226	9	US-09-929-955-10	Sequence 10, Appl
5	1040	95.9	226	13	US-10-104-966-10	Sequence 10, Appl
6	1040	95.9	226	15	US-10-719-619-10	Sequence 10, Appl
7	1040	95.9	226	16	US-10-817-591-10	Sequence 10, Appl
8	1040	95.9	227	16	US-10-472-724-27	Sequence 27, Appl
9	1040	95.9	249	15	US-10-371-525-16	Sequence 16, Appl
10	1040	95.9	249	15	US-10-371-069-16	Sequence 16, Appl
11	1040	95.9	249	15	US-10-371-645-16	Sequence 16, Appl
12	1040	95.9	249	15	US-10-371-260-16	Sequence 16, Appl
13	1040	95.9	281	9	US-09-247-890-12	Sequence 12, Appl
14	1040	95.9	281	15	US-10-383-317-12	Sequence 12, Appl
15	1040	95.9	334	16	US-10-472-724-10	Sequence 10, Appl
16	1040	95.9	389	15	US-10-267-682-106	Sequence 106, App
17	1040	95.9	389	15	US-10-267-748-106	Sequence 106, App
18	1040	95.9	397	9	US-09-812-862-6	Sequence 6, Appli
19	1033	95.2	226	9	US-09-812-862-14	Sequence 14, Appl
20	1033	95.2	389	9	US-09-821-877-2	Sequence 2, Appli
21	1033	95.2	389	16	US-10-847-493-2	Sequence 2, Appli
22	1032	95.1	229	9	US-09-821-877-8	Sequence 8, Appli
23	1032	95.1	229	16	US-10-847-493-8	Sequence 8, Appli
24	1026	94.6	305	18	US-10-911-464B-30	Sequence 30, Appl
25	1007	92.8	226	17	US-10-838-834-14	Sequence 14, Appl
26	1007	92.8	281	18	US-10-715-665-3	Sequence 3, Appli
27	1007	92.8	390	18	US-10-715-665-5	Sequence 5, Appli
28	1007	92.8	454	17	US-10-912-969-38	Sequence 38, Appl
29	1007	92.8	531	18	US-10-715-665-7	Sequence 7, Appli
30	1007	92.8	678	15	US-10-365-620-29	Sequence 29, Appl
31	1007	92.8	678	15	US-10-365-620-32	Sequence 32, Appl
32	1007	92.8	678	17	US-10-912-969-36	Sequence 36, Appl
33	1007	92.8	678	17	US-10-913-171-29	Sequence 29, Appl
34	991	91.3	226	15	US-10-335-774-2	Sequence 2, Appli
35	991	91.3	226	15	US-10-335-774-40	Sequence 40, Appl
36	988	91.1	400	15	US-10-411-037-46	Sequence 46, Appl
37	988	91.1	400	15	US-10-411-026-46	Sequence 46, Appl
38	988	91.1	400	15	US-10-410-962-46	Sequence 46, Appl
39	988	91.1	400	15	US-10-411-049-46	Sequence 46, Appl
40	988	91.1	400	16	US-10-410-930-46	Sequence 46, Appl
41	988	91.1	400	16	US-10-410-997-46	Sequence 46, Appl
42	988	91.1	400	16	US-10-411-012-46	Sequence 46, Appl
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ALIGNMENTS

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; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; TITLE OF INVENTION: CONSTITUENTS AND USES THEREOF
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match 96.4%; Score 1046; DB 14; Length 226;
Best Local Similarity 95.8%; Pred. No. 1.9e-82;
Matches 181; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 25, 2005, 11:24:37 ; Search time 156 Seconds
(without alignments)
471.279 Million cell updates/sec

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Perfect score: 1085
Sequence: 1 DSWWTSLNFLGGTTVCLGQN.....GPSLYSILSPFSPLLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1046	96.4	226	14	US-10-169-668-5	Sequence 5, Appli
2	1046	96.4	389	14	US-10-169-668-6	Sequence 6, Appli
3	1043	96.1	226	18	US-10-911-464B-36	Sequence 36, Appl
4	1040	95.9	226	9	US-09-929-955-10	Sequence 10, Appl
5	1040	95.9	226	13	US-10-104-966-10	Sequence 10, Appl
6	1040	95.9	226	15	US-10-719-619-10	Sequence 10, Appl
7	1040	95.9	226	16	US-10-817-591-10	Sequence 10, Appl
8	1040	95.9	227	16	US-10-472-724-27	Sequence 27, Appl
9	1040	95.9	249	15	US-10-371-525-16	Sequence 16, Appl
10	1040	95.9	249	15	US-10-371-069-16	Sequence 16, Appl
11	1040	95.9	249	15	US-10-371-645-16	Sequence 16, Appl
12	1040	95.9	249	15	US-10-371-260-16	Sequence 16, Appl
13	1040	95.9	281	9	US-09-247-890-12	Sequence 12, Appl
14	1040	95.9	281	15	US-10-383-317-12	Sequence 12, Appl
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16	1040	95.9	389	15	US-10-267-682-106	Sequence 106, App
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18	1040	95.9	397	9	US-09-812-862-6	Sequence 6, Appli
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21	1033	95.2	389	16	US-10-847-493-2	Sequence 2, Appli
22	1032	95.1	229	9	US-09-821-877-8	Sequence 8, Appli
23	1032	95.1	229	16	US-10-847-493-8	Sequence 8, Appli
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25	1007	92.8	226	17	US-10-838-834-14	Sequence 14, Appl
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28	1007	92.8	454	17	US-10-912-969-38	Sequence 38, Appl
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32	1007	92.8	678	17	US-10-912-969-36	Sequence 36, Appl
33	1007	92.8	678	17	US-10-913-171-29	Sequence 29, Appl
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42	988	91.1	400	16	US-10-411-012-46	Sequence 46, Appl
43	988	91.1	400	16	US-10-287-994-46	Sequence 46, Appl
44	988	91.1	400	16	US-10-410-913-46	Sequence 46, Appl
45	988	91.1	400	17	US-10-410-980-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; TITLE OF INVENTION: CONSTITUENTS AND USES THEREOF
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match 96.4%; Score 1046; DB 14; Length 226;
Best Local Similarity 95.8%; Pred. No. 1.9e-82;
Matches 181; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | ||||||||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| ||||||||||||||||||||||||:|| ||
```

```
Db        213 LPLLPIFFC 221


RESULT 5
US-10-104-966-10
; Sequence 10, Application US/10104966
; Publication No. US20020155124A1
; GENERAL INFORMATION:
;  APPLICANT: Matti Sallberg
;  APPLICANT:  Catharina Hultgren
;  TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: TRIPEP.23AUSC1
;  CURRENT APPLICATION NUMBER: US/10/104,966
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/705,547
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/229,175
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-10-104-966-10

  Query Match             95.9%;  Score 1040;  DB 13;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 6.3e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 6
US-10-719-619-10
; Sequence 10, Application US/10719619
; Publication No. US20040086529A1
; GENERAL INFORMATION:
;  APPLICANT: Matti Sallberg
;  APPLICANT:  Catharina Hultgren
;  TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: TRIPEP.23AUSC1C
;  CURRENT APPLICATION NUMBER: US/10/719,619
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 10/104,966
;  PRIOR FILING DATE: 2002-03-22
;  PRIOR APPLICATION NUMBER: 09/705,547
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/229,175
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-10-719-619-10

  Query Match             95.9%;  Score 1040;  DB 15;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 6.3e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221


RESULT 7
US-10-817-591-10
; Sequence 10, Application US/10817591
; Publication No. US20040229832A1
; GENERAL INFORMATION:
;  APPLICANT: Matti Sallberg
;  APPLICANT:  Catharina Hultgren
;  TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: TRIPEP.23AUS2C1
;  CURRENT APPLICATION NUMBER: US/10/817,591
;  CURRENT FILING DATE:  2004-04-02
;  PRIOR APPLICATION NUMBER: 10/719,619
;  PRIOR FILING DATE: 2003-11-20
;  PRIOR APPLICATION NUMBER: 10/104,966
;  PRIOR FILING DATE: 2002-03-22
;  PRIOR APPLICATION NUMBER: 09/929,955
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: 09/705,547
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/229,175
;  PRIOR FILING DATE: 2000-08-29
;  PRIOR APPLICATION NUMBER: 60/225,767
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-10-817-591-10

  Query Match             95.9%;  Score 1040;  DB 16;  Length 226;
  Best Local Similarity   95.8%;  Pred. No. 6.3e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
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                ||||||||:|||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
                  |||||||||
Db        213 LPLLPIFFC 221


RESULT 8
US-10-472-724-27
; Sequence 27, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
;  APPLICANT: Cid-Arregui, Angel
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
;  FILE REFERENCE: 4121-154
;  CURRENT APPLICATION NUMBER: US/10/472,724
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/EP02/03271
;  PRIOR FILING DATE: 2002-03-22
;  PRIOR APPLICATION NUMBER: EP 01107271.7
;  PRIOR FILING DATE: 2001-03-23
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 227
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic gene EHBs Ag-S-F
US-10-472-724-27

  Query Match             95.9%;  Score 1040;  DB 16;  Length 227;
  Best Local Similarity   95.8%;  Pred. No. 6.3e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 91

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:||||||||||||| | |||| | |||||||||||||||||||||||||
Db         92 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 151

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| |||||||||||||||||||||||||||||||||||||
Db        152 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 211

Qy        181 SPLLPIFFC 189
                  |||||||||
Db        212 LPLLPIFFC 220


RESULT 9
US-10-371-525-16
; Sequence 16, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/10/371,525
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/311,784
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-HBV-s
US-10-371-525-16

  Query Match             95.9%;  Score 1040;  DB 15;  Length 249;
  Best Local Similarity   95.8%;  Pred. No. 6.9e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 115

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:||||||||||||| | |||| | |||||||||||||||||||||||||
Db        116 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 175

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||| |||||||||||||||||||||||||||||||||||||
Db        176 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 235

Qy        181 SPLLPIFFC 189
                  |||||||||
Db        236 LPLLPIFFC 244


RESULT 10
US-10-371-069-16
; Sequence 16, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE Inc.
;  APPLICANT:  Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.10
;  CURRENT APPLICATION NUMBER: US/10/371,069
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/078,904
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-HBV-s
US-10-371-069-16

  Query Match             95.9%;  Score 1040;  DB 15;  Length 249;
  Best Local Similarity   95.8%;  Pred. No. 6.9e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 115
```

```
Qy          61 PLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
               ||||||||||:||||||||||||||| | |||| | ||||||||||||||||||||||||
Db         116 PLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 175

Qy         121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
               ||||||||:||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         176 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 235

Qy         181 SPLLPIFFC 189
               |||||||||
Db         236 LPLLPIFFC 244


RESULT 11
US-10-371-645-16
; Sequence 16, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE Inc.
;  APPLICANT:  Pikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.11
;  CURRENT APPLICATION NUMBER: US/10/371,645
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US 09/078,904
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-HBV-s
US-10-371-645-16

  Query Match           95.9%;  Score 1040;  DB 15;  Length 249;
  Best Local Similarity  95.8%;  Pred. No. 6.9e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          56 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 115

Qy          61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
               ||||||||||:||||||||||||||| | |||| | ||||||||||||||||||||||||
Db         116 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 175

Qy         121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
               ||||||||:||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         176 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 235

Qy         181 SPLLPIFFC 189
               |||||||||
Db         236 LPLLPIFFC 244


RESULT 12
US-10-371-260-16
; Sequence 16, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE Inc.
;  APPLICANT:  Pikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.13
;  CURRENT APPLICATION NUMBER: US/10/371,260
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/078,904
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-HBV-s
US-10-371-260-16

  Query Match           95.9%;  Score 1040;  DB 15;  Length 249;
  Best Local Similarity  95.8%;  Pred. No. 6.9e-82;
  Matches  181;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          56 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 115

Qy          61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
               ||||||||||:||||||||||||||| | |||| | ||||||||||||||||||||||||
Db         116 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 175

Qy         121 PSSWAPGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
               ||||||||:||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         176 PSSWAPGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 235

Qy         181 SPLLPIFFC 189
               |||||||||
Db         236 LPLLPIFFC 244


RESULT 13
US-09-247-890-12
; Sequence 12, Application US/09247890
; Publication No. US20020198162A1
; GENERAL INFORMATION:
;  APPLICANT: Punnonen, Juha
;  APPLICANT: Bass, Steven H.
;  APPLICANT: Whalen, Robert Gerald
;  APPLICANT: Howard, Russell
;  APPLICANT: Stemmer, Willem P.C.
;  APPLICANT: Maxygen, Inc.
;  TITLE OF INVENTION: Antigen Library Immunization
;  FILE REFERENCE: 018097-028710US
;  CURRENT APPLICATION NUMBER: US/09/247,890
;  CURRENT FILING DATE: 1999-02-10
;  EARLIER APPLICATION NUMBER: US 60/074,294
;  EARLIER FILING DATE: 1998-02-11
;  EARLIER APPLICATION NUMBER: US 60/105,509
;  EARLIER FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Hepatitis B virus
US-09-247-890-12
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Query Match 95.9%; Score 1040; DB 9; Length 281;
Best Local Similarity 95.8%; Pred. No. 7.8e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
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Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
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Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
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Db        268 LPLLPIFFC 276
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RESULT 14
US-10-383-317-12
; Sequence 12, Application US/10383317
; Publication No. US20040001849A1
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juha
; APPLICANT: Bass, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/10/383,317
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/247,890
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-383-317-12

Query Match 95.9%; Score 1040; DB 15; Length 281;
Best Local Similarity 95.8%; Pred. No. 7.8e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 147

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db        148 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 207

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        208 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 267

Qy        181 SPLLPIFFC 189
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Db        268 LPLLPIFFC 276
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; Sequence 10, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-10

Query Match 95.9%; Score 1040; DB 16; Length 334;
Best Local Similarity 95.8%; Pred. No. 9.2e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLLCLI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 DSWWTSLNFLGGTTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLI 92

Qy         61 FLLVLLDYQGILPVCPLIPGSSTTSKGQCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPI 120
              ||||||||||:|||||||||||||| | |||| | ||||||||||||||||||||||||||
Db         93 FLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPI 152

Qy        121 PSSWAFGKYLWEWASARFSWLSSLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 180
              ||||||||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        153 PSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPF 212

Qy        181 SPLLPIFFC 189
              |||||||||
Db        213 LPLLPIFFC 221
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Search completed: July 25, 2005, 11:38:01
Job time : 158 secs